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U.S. APPLICATION NUMBER NO.	FIRST NAMED APPLICANT	ATTY. DOCKET NO.
10/592,944	Cécile BOUGERET	0510-1149

INTERNATIONAL APPLICATION NO.	
PCT/FR05/50165	

I.A. FILING DATE	PRIORITY DATE
03/15/2005	03/16/2004

466
YOUNG & THOMPSON
745 SOUTH 23RD STREET
2ND FLOOR
ARLINGTON, VA 22202

CONFIRMATION NO. 8660
371 FORMALITIES LETTER

OC000000025332239

Date Mailed: 08/13/2007

NOTIFICATION TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

Applicant is cautioned that correction of the above items may cause the specification and drawings page count to exceed 100 pages. If the specification and drawings exceed 100 pages, applicant will need to submit the required application size fee.

For questions regarding compliance to 37 CFR 1.821-1.825 requirements, please contact:

- **For Rules Interpretation, call (571) 272-0951**
- **For Patentin Software Program Help, call Patent EBC at 1-866-217-9197 or directly at 703-305-3028 / 703-308-6845 between the hours of 6 a.m. and 12 midnight, Monday through Friday, EST.**
- **Send e-mail correspondence for Patentin Software Program Help @ ebc@uspto.gov**

Applicant is reminded that any communications to the United States Patent and Trademark Office must be mailed to the address given in the heading and include the U.S. application no. shown above (37 CFR 1.5)

Registered users of EFS-Web may alternatively submit their reply to this notice via EFS-Web. https://sportal.uspto.gov/authenticate/AuthenticateUserLocalEPF.html

For more information about EFS-Web please call the USPTO Electronic Business Center at **1-866-217-9197** or visit our website at http://www.uspto.gov/ebc.

If you are not using EFS-Web to submit your reply, you must include a copy of this notice.

FRANCINE YOUNG

Telephone: (703) 308-9140 EXT 215

PART 1 - ATTORNEY/APPLICANT COPY

U.S. APPLICATION NUMBER NO.	INTERNATIONAL APPLICATION NO.	ATTY. DOCKET NO.
10/592,944	PCT/FR05/50165	0510-1149

FORM PCT/DO/EO/922 (371 Formalities Notice)

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/592,944_

Source: _1FwP_

Date Processed by STIC: _9/28/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE __CHECKER VERSION 4.4.0 PROGRAM__, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/592,944_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length Sequence(s)_____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7_____Skipped Sequences
(OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences
(NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213>
Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11_____Use of <220> Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12_____PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____ Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – STIC Systems Branch – 03/02/06

use English in all the sequences in submitted file

see pp 1-5, 7

IFWP

RAW SEQUENCE LISTING   DATE: 09/28/2006
PATENT APPLICATION: US/10/592,944   TIME: 11:21:02

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\09282006\J592944.raw *use English for a U.S. application*

```
   3 <110> APPLICANT: CYTOMICS SYSTEMS
   5 <120> TITLE OF INVENTION: Procede de criblage in vitro d'agents modulant
   6       l'ubiquitination de la proteine I-Kappa-B-Alpha et
   7       moyens destines a la mise en oeuvre dudit procede
   9 <130> FILE REFERENCE: CYTOMICS
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/592,944
C--> 12 <141> CURRENT FILING DATE: 2006-09-15
  14 <160> NUMBER OF SEQ ID NOS: 25
  16 <170> SOFTWARE: PatentIn Ver. 2.1
```

see item 4 on Euro summary sheet

ERRORED SEQUENCES

Per 1.824 d) Sequence Rules, a label MUST be on computer readable form

Does Not Comply Corrected Diskette Needed

```
  18 <210> SEQ ID NO: 1
  19 <211> LENGTH: 1719
E--> 20 <212> TYPE: ADN  DNA
C--> 21 <213> ORGANISM: Sequence artificielle   use English
  23 <220> FEATURE:
  24 <223> OTHER INFORMATION: Description de la sequence
  25       artificielle GFP-NLS-IkBa
```

insufficient explanation - give source of genetic material - see item 11 on Euro summary sheet

```
  27 <400> SEQUENCE: 1
  28 atgtctaaag gtgaagaatt attcactggt gttgtcccaa ttttggttga attagatggt 60
  29 gatgttaatg gtcacaaatt ttctgtctcc ggtgaaggtg aaggtgatgc tacttacggt 120
  30 aaattgacct taaaatttat ttgtactact ggtaaattgc cagttccatg gccaacctta 180
  31 gtcactactt tcggttatgg tgttcaatgt tttgctagat acccagatca tatgaaacaa 240
  32 catgactttt tcaagtctgc catgccagaa ggttatgttc aagaaagaac tatttttttc 300
  33 aaagatgacg gtaactacaa gaccagagct gaagtcaagt ttgaaggtga taccttagtt 360
  34 aatagaatcg aattaaaagg tattgatttt aaagaagatg gtaacatttt aggtcacaaa 420
  35 ttggaataca actataactc tcacaatgtt tacatcatgg ctgacaaaca aaagaatggt 480
  36 atcaaagtta acttcaaaat tagacacaac attgaagatg gttctgttca attagctgac 540
  37 cattatcaac aaaatactcc aattggtgat ggtccagtct tgttaccaga caaccattac 600
  38 ttatccactc aatctgcctt atccaaagat ccaaacgaaa agagagacca catggtcttg 660
  39 ttagaatttg ttactgctgc tggtattacc catggtatgg atgaattgta caaactgcag 720
  40 agcccacctc caaaaaagaa gagaaaggtc gaattgggcg gatccatgtt ccaggcggcc 780
  41 gagcgccccc aggagtgggc catggagggc ccccgcgacg ggctgaagaa ggagcggcta 840
  42 ctggacgacc gccacgacag cggcctggac tccatgaaag acgaggagta cgagcagatg 900
  43 gtcaaggagc tgcaggagat ccgcctcgag ccgcaggagg tgccgcgcgg ctcggagccc 960
  44 tggaagcagc agctcaccga ggacggggac tcgttcctgc acttggccat catccatgaa 1020
  45 gaaaaggcac tgaccatgga agtgatccgc caggtgaagg gagacctggc tttcctcaac 1080
  46 ttccagaaca acctgcagca gactccactc cacttggctg tgatcaccaa ccagccagaa 1140
  47 attgctgagg cacttctggg agctggctgt gatcctgagc tccgagactt tcgaggaaat 1200
  48 accccctac accttgcctg tgagcagggc tgcctggcca gcgtgggagt cctgactcag 1260
  49 tcctgcacca ccccgcacct ccactccatc ctgaaggcta ccaactacaa tggccacacg 1320
```

Please correct this error in subsequent sequences too.

```
 50 tgtctacact tagcctctat ccatggctac ctgggcatcg tggagctttt ggtgtccttg 1380
 51 ggtgctgatg tcaatgctca ggagccctgt aatggccgga ctgcccttca cctcgcagtg 1440
 52 gacctgcaaa atcctgacct ggtgtcactc ctgttgaagt gtggggctga tgtcaacaga 1500
 53 gttacctacc agggctattc tccctaccag ctcacctggg gccgcccaag cacccggata 1560
 54 cagcagcagc tgggccagct gacactagaa aaccttcaga tgctgccaga gagtgaggat 1620
 55 gaggagagct atgacacaga gtcagagttc acgagttca cagaggacga gctgccctat 1680
 56 gatgactgtg tgtttggagg ccagcgtctg acgttatga                        1719
179 <210> SEQ ID NO: 3
180 <211> LENGTH: 2583
181 <212> TYPE: ADN DNA
182 <213> ORGANISM: Sequence artificielle   use English
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Description de la sequence   insufficient explanation
186       artificielle:GFP-NLS-bTRCP
188 <400> SEQUENCE: 3
189 atgtctaaag gtgaagaatt attcactggt gttgtcccaa ttttggttga attagatggt 60
190 gatgttaatg gtcacaaatt ttctgtctcc ggtgaaggtg aaggtgatgc tacttacggt 120
191 aaattgacct taaaatttat ttgtactact ggtaaattgc cagttccatg gccaacctta 180
192 gtcactactt tcggttatgg tgttcaatgt tttgctagat acccagatca tatgaaacaa 240
193 catgacttt tcaagtctgc catgccagaa ggttatgttc aagaaagaac tatttttttc 300
194 aaagatgacg gtaactacaa gaccagagct gaagtcaagt ttgaaggtga taccttagtt 360
195 aatagaatcg aattaaaagg tattgatttt aaagaagatg gtaacatttt aggtcacaaa 420
196 ttggaataca actataactc tcacaatgtt tacatcatgg ctgacaaaca aaagaatggt 480
197 atcaaagtta acttcaaaat tagacacaac attgaagatg gttctgttca attagctgac 540
198 cattatcaac aaaatactcc aattggtgat ggtccagtct tgttaccaga caaccattac 600
199 ttatccactc aatctgcctt atccaaagat ccaaacgaaa agagagacca catggtcttg 660
200 ttagaatttg ttactgctgc tggtattacc catggtatgg atgaattgta caaactgcag 720
201 agcccacctc caaaaaagaa gagaaaggtc gaattgggcg gatccatgga cccggccgag 780
202 gcggtgctgc aagagaaggc actcaagttt atgtgctcta tgcccaggtc tctgtggctg 840
203 ggctgctcca gcctggcgga cagcatgcct tcgctgccgat gcctgtataa cccagggact 900
204 ggcgcactca cagctttcca gaattcctca gagagagaag actgtaataa tggcgaaccc 960
205 cctaggaaga taataccaga gaagaattca cttagacaga catacaacag ctgtgccaga 1020
206 ctctgcttaa accaagaaac agtatgttta gcaagcactg ctatgaagac tgagaattgt 1080
207 gtggccaaaa caaaacttgc caatggcact tccagtatga ttgtgcccaa gcaacggaaa 1140
208 ctctcagcaa gctatgaaaa ggaaaaggaa ctgtgtgtca aatactttga gcagtggtca 1200
209 gagtcagatc aagtggaatt tgtggaacat cttatatccc aaatgtgtca ttaccaacat 1260
210 gggcacataa actcgtatct taaacctatg ttgcagagag atttcataac tgctctgcca 1320
211 gctcggggat tggatcatat tgctgagaac attctgtcat acctggatgc caaatcacta 1380
212 tgtgctgctg aacttgtgtg caaggaatgg taccgagtga cctctgatgg catgctgtgg 1440
213 aagaagctta tcgagagaat ggtcaggaca gattctctgt ggagaggcct ggcagaacga 1500
214 agaggatggg gacagtattt attcaaaaac aaacctcctg acgggaatgc tcctcccaac 1560
215 tcttttttata gagcacttta tcctaaaatt atacaagaca ttgagacaat agaatctaat 1620
216 tggagatgtg aagacatag tttacagaga attcactgcc gaagtgaaac aagcaaagga 1680
217 gtttactgtt tacagtatga tgatcagaaa atagtaagcg gccttcgaga caacacaatc 1740
218 aagatctggg ataaaaacac attggaatgc aagcgaattc tcacaggcca tacaggttca 1800
219 gtcctctgtc tccagtatga tgagagagtg atcataacag gatcatcgga ttccacggtc 1860
220 agagtgtggg atgtaaatac aggtgaaatg ctaaacacgt tgattcacca ttgtgaagca 1920
221 gttctgcact tgcgtttcaa taatggcatg atggtgacct gctccaaaga tcgttccatt 1980
222 gctgtatggg atatggcctc cccaactgac attaccctcc ggagggtgct ggtcggacac 2040
```

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\09282006\J592944.raw

```
223 cgagctgctg tcaatgttgt agactttgat gacaagtaca ttgtttctgc atctgggat 2100
224 agaactataa aggtatggaa cacaagtact tgtgaatttg taaggacctt aaatggacac 2160
225 aaacgaggca ttgcctgttt gcagtacagg gacaggctgg tagtgagtgg ctcatctgac 2220
226 aacactatca gattatggga catagaatgt ggtgcatgtt tacgagtgtt agaaggccat 2280
227 gaggaattgg tgcgttgtat tcgatttgat aacaagagga tagtcagtgg ggcctatgat 2340
228 ggaaaaatta.aagtgtggga tcttgtggct gctttggacc cccgtgctcc tgcagggaca 2400
229 ctctgtctac ggacccttgt ggagcattcc ggaagagttt ttcgactaca gtttgatgaa 2460
230 ttccagattg tcagtagttc acatgatgac acaatcctca tctgggactt cctaaatgat 2520
231 ccagctgccc aagctgaacc cccccgttcc ccttctcgaa catacaccta catctccaga 2580
232 tga                                                              2583
409 <210> SEQ ID NO: 5
410 <211> LENGTH: 21
411 <212> TYPE: (ADN) DNA
412 <213> ORGANISM: Simian virus 40
414 <400> SEQUENCE: 5
415 ccaaaaaaga agagaaaggt c                                           21
418 <210> SEQ ID NO: 6
419 <211> LENGTH: 35
420 <212> TYPE: (ADN)
421 <213> ORGANISM: Sequence artificielle
423 <220> FEATURE:
424 <223> OTHER INFORMATION: Description de la sequence artificielle:Amorce
426 <400> SEQUENCE: 6
427 gctgggtacc ttaataatca tattacatgg catta                            35
430 <210> SEQ ID NO: 7
431 <211> LENGTH: 34
432 <212> TYPE: (ADN)
433 <213> ORGANISM: Sequence artificielle
435 <220> FEATURE:
436 <223> OTHER INFORMATION: Description de la sequence artificielle:Amorce
438 <400> SEQUENCE: 7
439 ggcggaattc tatagttttt ctccttgac gtta                              34
442 <210> SEQ ID NO: 8
443 <211> LENGTH: 35
444 <212> TYPE: (ADN)
445 <213> ORGANISM: Sequence artificielle
447 <220> FEATURE:
448 <223> OTHER INFORMATION: Description de la sequence artificielle:Amorce
450 <400> SEQUENCE: 8
451 ggtcggaatt catgtctaaa ggtgaagaat tattc                            35
454 <210> SEQ ID NO: 9
455 <211> LENGTH: 46
456 <212> TYPE: (ADN)
457 <213> ORGANISM: Séquence artificielle
459 <220> FEATURE:
460 <223> OTHER INFORMATION: Description de la sequence artificielle:Amorce
462 <400> SEQUENCE: 9
463 ggcgggatcc gcccgggctg tgcagtttgt acaattcatc catacc                46
466 <210> SEQ ID NO: 10
```

E--> (marks at 411, 420, 432, 444, 456)
C--> (marks at 421, 433, 445, 457)

Handwritten annotations: 1) use English 2) give source of ? genetic material

RAW SEQUENCE LISTING   DATE: 09/28/2006
PATENT APPLICATION: US/10/592,944   TIME: 11:21:02

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\09282006\J592944.raw

```
        467 <211> LENGTH: 44
E--> 468 <212> TYPE: ADN
C--> 469 <213> ORGANISM: Sequence artificielle
        471 <220> FEATURE:
        472 <223> OTHER INFORMATION: Description de la sequence artificielle:Amorce
        474 <400> SEQUENCE: 10
        475 ggcggcggcc gccaccgcgg tgggcgaatt tcttatgatt tatg          44
        478 <210> SEQ ID NO: 11
        479 <211> LENGTH: 30
E--> 480 <212> TYPE: ADN
C--> 481 <213> ORGANISM: Sequence artificielle
        483 <220> FEATURE:
        484 <223> OTHER INFORMATION: Description de la sequence artificielle:Amorce
        486 <400> SEQUENCE: 11
        487 ggcggagctc tggaagaacg attacaacag                          30
        490 <210> SEQ ID NO: 12
        491 <211> LENGTH: 30
E--> 492 <212> TYPE: ADN
C--> 493 <213> ORGANISM: Sequence artificielle
        495 <220> FEATURE:
        496 <223> OTHER INFORMATION: Description de la sequence artificielle:Amorce
        498 <400> SEQUENCE: 12
        499 acctccaaaa aagaagagaa aggtcgaatt                          30
        502 <210> SEQ ID NO: 13
        503 <211> LENGTH: 31
E--> 504 <212> TYPE: ADN
C--> 505 <213> ORGANISM: Sequence artificielle
        507 <220> FEATURE:
        508 <223> OTHER INFORMATION: Description de la sequence artificielle:Amorce
        510 <400> SEQUENCE: 13
        511 ggcgggtacc gtgagtaagg aaagagtgag g.                        31
        514 <210> SEQ ID NO: 14
        515 <211> LENGTH: 33
E--> 516 <212> TYPE: ADN
C--> 517 <213> ORGANISM: Sequence artificielle
        519 <220> FEATURE:
        520 <223> OTHER INFORMATION: Description de la sequence artificielle:Amorce
        522 <400> SEQUENCE: 14
        523 ggcggaattc tgttttatat ttgttgtaaa aag                       33
        526 <210> SEQ ID NO: 15
        527 <211> LENGTH: 33
E--> 528 <212> TYPE: ADN
C--> 529 <213> ORGANISM: Sequence artificielle
        531 <220> FEATURE:
        532 <223> OTHER INFORMATION: Description de la sequence artificielle:Amorce
        534 <400> SEQUENCE: 15
        535 ggcggaattc atggactaca aagaccatga cgg                       33
        538 <210> SEQ ID NO: 16
        539 <211> LENGTH: 46
```

RAW SEQUENCE LISTING   DATE: 09/28/2006
PATENT APPLICATION: US/10/592,944   TIME: 11:21:02

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\09282006\J592944.raw

```
E--> 540 <212> TYPE  ADN
C--> 541 <213> ORGANISM: Sequence artificielle
     543 <220> FEATURE:
     544 <223> OTHER INFORMATION: Description de la sequence artificielle:Amorce
     546 <400> SEQUENCE: 16
     547 ggcgggatcc gcccgggctc tgcagcttgt catcgtcatc cttgta                46
     680 <210> SEQ ID NO: 25
     681 <211> LENGTH: 30
E--> 682 <212> TYPE: ADN
C--> 683 <213> ORGANISM: Sequence artificielle
     685 <220> FEATURE:
     686 <223> OTHER INFORMATION: Description de la sequence artificielle:Amorce
     688 <400> SEQUENCE: 25
     689 aattcgacct ttctcttctt ttttggaggt                30
     695 1
```

delete

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/592,944

DATE: 09/28/2006
TIME: 11:21:03

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\09282006\J592944.raw

L = 11 M:270 C: Current Application Number differs, Replaced Application Number
L = 12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L = 20 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:1
L = 21 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L = 62 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L = 181 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:3
L = 182 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L = 238 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L = 411 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:5
L = 420 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:6
L = 421 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L = 432 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:7
L = 433 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L = 444 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:8
L = 445 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L = 456 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:9
L = 457 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L = 468 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:10
L = 469 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L = 480 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:11
L = 481 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L = 492 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:12
L = 493 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L = 504 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:13
L = 505 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L = 516 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:14
L = 517 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L = 528 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:15
L = 529 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L = 540 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:16
L = 541 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L = 553 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L = 567 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L = 581 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L = 598 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L = 612 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L = 626 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L = 643 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L = 669 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L = 682 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:25
L = 683 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25

```
<210> 17
<211> 9
<212> PRT
<213> Sequence artificielle
```
→ use English

```
<220>
<223> Description de la sequence artificielle HA
```
? give source of genetic material

```
<400> 17
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
 1               5
```

(please explain source of genetic material in all Artificial Sequences)